GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd. Copyright

OM protein - protein search, using sw model

April Run on:

6, 2005, 06:11:39; Search time 93 Seconds (without alignments) 897.515 Million cell updates/sec

US-10-616-410-2 852 1 MADREKLPPGWEKRMSRSSG......GEMSGPVFTDSGIHIILRTE 163 Title: Perfect score:

Scoring table:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

1612378 segs, 512079187 residues Searched:

1612378 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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. uo	3526 homo sap qur7 mus musc	Q9i9k6 xenopus lae	management 1	Q6azr5 xenopus lae O6nbx1 brachydanio		drogophila		Olivy, neurospora O60045 neurospora	Ņ	10	schizosac	. Q6cel8 yarrowia li	3 kluyvero	Q9c475 candida alb	O		0	Ü	dictyost	ಹ	ab7 anophel	Q98142 arabidopsis	428 homo sapi	0 malus	Q9lek8 digitalis l	0 oryza ga	1rj5
SUMMARIES	PIN1_HUMAN PIN1_MOUSE	Q919 <u>K</u> 6 O642N3	Q6DEE1	Q6AZR5 Q6PBX1	Q7QAB6	\mathbf{c}	09N492	SSP1 NEUCR	Q6UAY2	042735	PIN1_SCHPO	Q6CEL8	Q6CMZ3	Q9C475	OBNJNS	QGBRV8	ESS1_YEAST	Oerrp9	P90527	Q75CN9	Q7QAB7	PINI ARATH	PINL HUMAN	PIN1_MALDO	PIN1_DIGLA	E+	QBIRJS
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ALIGNMENTS

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collaboration
                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                       peptidylproline
        cis/trans
                                                                                                                                                                                                                                     N-T
                                               family
activity. Displays a preference for an acidic residue N-to the isomerized proline bond. Catalyzing pSer/Thr-Proisomerizations.
CATALYTIC ACTIVITY: Peptidylproline (omega=180) = peptid
                                                rotamase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35391AF40B7D1E13
                                (omega=0).
SUBCELLULAR LOCATION: Nuclear.
SIMILARITY: Belongs to the ppiC/parvulin
SIMILARITY: Contains 1 WW domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   L61
18243 MW;
                                                                                                                                              .1;
                                                                                                                                    EMBL; U49070; AAC50492.1; -
EMBL; BC002899; AAH02899.1;
PIR; S68520; S68520.
PDB; 1F8A; X-ray; B=1-163.
PDB; 116C; NMR; A=6-44.
PDB; 118G; NMR; B=6-44.
PDB; 118H; NMR; B=6-44.
PDB; 1NMV; NMR; A=1-163.
PDB; 1NMW; NMR; A=1-163.
PDB; 1NMW; NMR; A=1-163.
                                                                                                                                                                                                              A=1-:
                                                                                                                                                                                                              PDB; 1PIN; X-ray; A=1
Genew; HGNC:8988; PIN:
H-InvDB; HIX0014730;
MIM; 601052; -.
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SEQUENCE FROW N.A.

STRAING-CS7BL/6J, TISSUE-Embryo, and Kidney;

MEDLINE-22354683; PubMed=12466851; DOI=10.1038/nature01266;

MARDLINE-22354683; PubMed=12466851; DOI=10.1038/nature01266;

MARDLINE-22354683; PubMed=12466851; DOI=10.1038/nature01266;

MARDLINE-22354683; PubMed=12466851; DOI=10.1038/nature01266;

MARDLINE-22354683; PubMed=12466851; DOI=10.1038/nature01266;

MARDLINE-CAPALY Garloon N., Salto R., Schombach C., Golobori T.,

MARDLINE D., Brade N., Matsuda H., Baralov S., Beisel K.W.,

MARDLINE D., Brade C., Chothia C., Corbani L.E., Cousins S.,

MARDLINE D., Brade C., Chothia C., Corbani L.E., Cousins S.,

MARDLINE D., Brade C., Hurcher C.P., Forrest A., Gough J.,

MARDLINE D., Marchion L., Mackson I.J., Jarvis E.D.,

MARDLINE MARDLINE D., Marchionni L., McKenzie L., Miki H.,

MARDLINE MARDLINE C., Semple C., Semple C., Ramachandran S.,

MARDLINE R., Pontius J.U., Qi D., Ramachandran S.,

MARDLINE R., Madlested C., Semple C.A., Setou M., Shimada K.,

MILLANA R., Takenaka Y., Taylor M.S., Teasfale R.D., Tomita N.,

MILLANE C., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,

Yuan Z., Zavolan M., Zhu Y., Zimmer A., Garninci P., Hayatsu N.,

Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,

Milmiki T., Waki K., Kawai J., Alzawa K., Atakawa T., Fukuda S.,

Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,

Miyazaki A., Sakai K., Saaaki D., Shibata K., Shinagawa A.,

Marne M., Sokanizaki Y.,

Masunishi A., Yoshino W., Intoh M., Kagawa I.,

Miyazaki A., Sakai Y.,

Masunishi A., Sokaini Y.,

Masunishi A., Yoshino W.,

Marne E.S., Shinagawa A.,

Marney E., Havashizaki Y.,

Mayaraki Y.,

Mayarak
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"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: Bssential PPIase that regulates mitosis presumably by interacting with NIMA and attenuating its mitosis-promoting activity. Displays a preference for an acidic residue N-terminal to the isomerized proline bond. Catalyzing pSer/Thr-Pro cis/trans isomerizations (By similarity).
LVKHSOSRRPSSWROEKITRTKBEALELINGYIOKIKSGEEDFESLASOFSDCSSAKARG
                                                                                                                         Tomita M.,
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MEDLINE=20070807; PubMed=10600477; DOI=10.1006/bbrc.1999.1736;
Fujimori F., Takahashi K., Uchida C., Uchida T.;
"Mice lacking Pin1 develop normally, but are defective in entering cell cycle from GO arrest.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                             163
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                                                                                                                                                                                                                                                                                                                                                                                                           28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Peptidyl-prolyl cis-trans isomerase NIMA-interacting (Rotamase Pinl) (PPIase Pinl).
                                                                                                                                                                                                                    DIGAFSRGOMOKPFEDASFALRTGEMSGPVFTDSGIHIILRTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biochem. Biophys. Res. Commun. 265:658-663(1999).
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                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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28-FEB-2003
28-FEB-2003
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                                                                                                                                               61
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Gaps

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163;

Length

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Score 852; D Pred. No. 3e-; Mismatches

100.0%;

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Conservative

Local Similarity hes 163; Conser

Query Match Best Local S Matches 163

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287:1644-1647(2000)
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NCBL_TaxID=8364;
                                                                                                                                                                                                                                                               SM00456;
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25-OCT-2004
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25-OCT-2004
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PRINTS;
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                                                                                                 88
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                                                                                                                    collaboration
                                                                                                                                                                                                   commercial
                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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   peptidylproline
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleost
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae,
Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=20165035; PubMed=10698738; DOI=10.1126/science.287.54
Winkler K.B., Swenson K.I., Kornbluth S., Means A.R.;
"Requirement of the prolyl isomerase Pinl for the replication
                  (omega=0).
SUBCELLULAR LOCATION: Nuclear (By similarity).
SIMILARITY: Belongs to the ppiC/parvulin rotamase family
SIMILARITY: Contains 1 WW domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MADEEKL PPGWEKRMSRSSGRVYY FNHI TNASOWER PSGNSSSGG--KNGO
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                                                                                                                                                                                                                                                                                                                                                                                                                          of cell proliferation; IMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF0039/; ...,
SMART; SM00456; WW; 1.
PROSITE; PS01096; PPIC_PPIASE_1; 1.
PROSITE; PS50198; PPIC_PPIASE_2; 1.
PROSITE; PS50159; WW_DOMAIN_1; 1.
PROSITE; PS50020; WW_DOMAIN_2; 1.
PROSITE; PS50020; WW_DOMAIN_2; 1.
Cell cycle; Isomerase; Nuclear protein; Rotamase.
DOMAIN 5 39 WW.
54 165 Ppic.
CATALYTIC ACTIVITY: Peptidylproline (omega=180)
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 814; DB 1; ]
Pred. No. 9.4e-67;
3; Mismatches 3;
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                                                                                                                                                                                                                                                                        EMBL; AB009691; BAA87037.1; -.
EMBL; AB009692; BAA87038.1; -.
EMBL; AK003369; BAB22743.1; -.
EMBL; AK002665; BAB22270.1; -.
PIR; JC7136; JC7136.
HSSP; Q13526; 1F8A.
MGD; MGI:1346036; Fin1.
GO; GO:0042127; P:regulation of ce.
InterPro; IPR000297; Rotamase.
InterPro; IPR001202; WW_RSp5_WWP.
Pfam; PF00639; Rotamase; 1.
Pfam; PF00639; WW; 1.
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il Similarity 95.2%;
157; Conservative
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01-JUN-2003 (TrEMBLre)
Prolyl isomerase Pinl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        checkpoint.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q919K6
Q919K6;
01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=Pin1;
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Best Local
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120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LVKHSQSRRPSSWRQEKITRTKEEALELINGYIQKIKSGEEDPESLASQFSDCSSAKARG
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Yelmode 12477932; DOI=10.1073/pnas.242603899;

Rtausherg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Rtausherg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Rtausher R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Robak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.B.,

Jones S.J., Marra M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MADERICLPPGWEKRMSRSSGRVYYFNHITNASQWERPSGNSSSGGKNGQGEPARVRCSHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S.J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                 activity;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 159;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CRC64;
                                                                               GO:0016853; F:1somerase activity; IEA.
GO:0003755; F:peptidyl-prolyl cis-trans isomerase
GO:0006457; P:protein folding; IEA.
to the ppiC/parvulin rotamase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DLGAPSRGOMOKPFEDASFALRTGEMSGPVFTDSGIHIILRTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4E54F66F16C9DF1C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88.4%; Score 753; DB 2;
87.1%; Pred. No. 3.6e-61
ive 11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS01096; PPIC PPIASE 1; 1
PROSITE; PS01096; PPIC PPIASE 2; 1
PROSITE; PS01159; WW DOMAIN 1; 1.
PROSITE; PS50020; WW DOMAIN 2; 1.
                                                                                                                                                                                                                        RBDS WWP
                                                                                                                                                              InterPro; IPR000297; Rotamase.
InterPro; IPR002349; WW.
InterPro; IPR001202; WW_Rsp5_W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17671 MW;
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-i- SIMILARITY: Bėlongs to 1
EMBL; AF239760; AAF43897.1;
HSSP; Q13526; 1F8A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 87.1%;
Matches 142; Conservative
                                                                                                                                                                                                                                               Pfam; PF00639; Rotamase; 1
Pfam; PF00397; WW; 1.
                                                                                                                                                                                                                                                                            700397; WW; 1.
PR00403; WWDOMAIN.
3M00456; WW; 1.
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                                                                                                                                                                                                                                                                                         57 LVKHNQSRRPSSWRQDRITRTKDBALEHINGYIQKIKSGDEDFESLASRFSDCSSAKAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-EMEDICS. FROM N.A:

TISSUE-EMEDICS.

A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.R., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.B.,

Jones S.J., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                      | :||||||
PGKVRCSHL
                                                                                                                                                                                                                                                                           CSSAKARG
                                                                                                                                                                                                                  PARVRCSHL
                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Embryo;
MBDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
Klein B.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein.
Xenopus laevis (African clawed frog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleos!
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Richardson P.; "Genetic and genomic tools for Xenopus research: The NIH Xenointiative.";
                                                                                                                                                                                                                                   1 MADERKLPPGWEKRMSRSSGRVYYPNHMTNASQWERP----TTGGKNGQGE
                                                                                                                                                                                                                                                                         LVICHSOSRRPSSWROEKITRTKERALELINGYIOKIKSGEEDFESLASOFS
                                                                                                                                                                                                                     MADEEKL PPGWEKRMSRSSGRVYY FNHI TNASOWER PSGNSSSGGKNGOGE
                                                                                                                                                             Length 159;
                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                           159
                                                                                       the EMBL/GenBank/DDBJ databases
                                                                                                                                 Al7A9C6C0E0AB858 CRC64;
                                                                                                                                                                                                                                                                                                                                DLGAFSRGOMOKPFEDASFALRTGEMSGPVFTDSGIHLILRTE
                                                                                                                                                                                                                                                                                                                                                28, Created)
28, Last sequence update)
28, Last annotation update)
and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
[2]
                                                                                                                                                , DB 2; Le
4.4e-61;
6;
                                                                                                                                                            score 752; DB Fred. No. 4.4e.
                                                                                                                                                                                                                                                                                                                                                                                                                                 159 AA
                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                17793 MW;
                                                           TISSUE=Embryo;
Klein S., Gerhard D.S.;
Submitted (AUG-2004) to the E
EMBL; BC081312; AAH81312.1; -
Hypothetical protein.
SEQUENCE 159 AA; 17793 MW;
                                                                                                                                                           88.3%;
nilarity 87.1%;
Conservative 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     initiative.";
Dev. Dyn. 225:384-391(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Xenopodinae; Xenopus.
NCBI_TaxID=8355;
                                                                                                                                                     Query Match
Best Local Similarity
Matches 142; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FROM N.A.
                                                 SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A
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25-0CT-2004
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                                                                                                                                                                                                                                                                                                                                                             117
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1 MADEEKLPPGWEKRMSRSSGRVYYFNHITNASQWERPSGNSSSGGKNGQGEPARVRCSHL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57 LVKHNQSRRPSSWRQDNITRTKDEALELINGYIQKIKSGDEDFESLASQFSDCSSAKAGG
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein (Fragment).
Xenopus laevis (African clawed frog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tools for Xenopus research: The NIH Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Lung;
PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Diatchenko L., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz
Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C
                                                                                                                                                                                                                                                                                                                                                                                                                              Length 159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOI=10.1002/dvdy.10174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                            CRC64;
                                                                                                           rotamase
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                   cecr4A870E316D3B
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                                                                                                                                                                                                                                                                                                                                                                                                                              Score 751; DB 2;
Pred. No. 5.4e-61;
2; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           158 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1132; PubMed=12454917; DOI=1
Strausberg R.L., Wagner L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                           SMART; SM00456; WW; 1.
PROSITE; PS01096; PPIC PPIASE 1;
PROSITE; PS50198; PPIC PPIASE 2;
PROSITE; PS01159; WW DOMAIN 1; 1
PROSITE; PS50020; WW DOMAIN 2; 1
Hypothetical protein; Isomerase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12;
U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                         17641 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                               88.1%;
86.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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159 AA; 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Lung;
MEDLINE=22341132;
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Acad.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TaxID=8355;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q6AZR5
Q6AZR5;
25-OCT-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      141;
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                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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116
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Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A. Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S. Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and initial analysis of more than 15,000 full-length human and initial analysis of more than 15,000 full-length human and initial analysis of more than 15,000 full-length human and initial analysis of more than 15,000 full-length human and initial analysis of more than 15,000 full-length human and initial analysis of more than 15,000 full-length human and initial analysis of more than 15,000 full-length human and initial analysis of more than 15,000 full-length human and initial analysis of more than 15,000 full-length human and initial analysis of more than 15,000 full-length human and initial analysis of more than 15,000 full-length human and initial analysis of more than 15,000 full-length human and initial analysis of more than 15,000 full-length human and initial analysis of more than 15,000 full-length human and initial analysis of more than 15,000 full-length human and initial analysis of more than 15,000 full-length human and initial analysis of more than 15,000 full-length human and initial analysis of more than 15,000 full-length analysis of more than 15,000 full-length analysis of more full-l
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein zgc:73206.
ORFNames=zgc:73206;
Brachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        G.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4
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                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

TISSUE=Lung;
Klein S., Strausberg R.;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
-1- SIMILARITY: Belongs to the ppiC/parvulin rotamase family EMBL; BC077447; AAH77447.1; -.
GO; GO:0016853; F:isomerase activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VKHSOSRRPSSWROEKITRTKERALELINGYIOKIKSGEEDFESLASOFSD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 158;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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Pred. No. 1e-60;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein; Isomerase; Rotamase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS01096; PPIC_PPIASE_1; 1
PROSITE; PS50198; PPIC_PPIASE_2; 1
PROSITE; PS01159; WW_DOMAIN_1; 1.
PROSITE; PS50020; WW_DOMAIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000297; Rotamase.
InterPro; IPR002349; WW.
InterPro; IPR001202; WW_Rsp5_WWP.
Pfam; PF00639; Rotamase; 1.
Pfam; PF00397; WW; 1.
PRINTS; PR00403; WWDOMAIN.
SMART; SM00456; WW; 1.
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87.0%;
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PRINTS; PR00403;
SMART; SM00456; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q6PBX1;
Q6PBX1;
05-JUL-2004
05-JUL-2004
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Best Local
Matches 14
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Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsleh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
A Jones S.J., Marra M.A.;
Reneration and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                     more than 15,000 full-length human
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles
NCBI_TaxID=180454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            activity; IEA
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rotamase family
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                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=Wild-type; TISSUE=Eye;
Strausberg R.;
Strausberg R.;
Strausberg R.;
Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
-1- SIMILARITY: Belongs to the ppiC/parvulin rotamase fam EMBL; BC059553; AAH59553.1; -.
ZFIN; ZDB-GENE-040426-1714; zgc:73206.
GO; GO:0016853; F:isomerase activity; IEA.
GO; GO:0006457; P:protein folding; IEA.
InterPro; IPR000297; Rotamase.
InterPro; IPR001202; WW_Rsp5_WWP.
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SMART; SM00456; Ww; 1.

PROSITE; PS01096; PPIC_PPIASE_1; 1.

PROSITE; PS01159; WW_DOMAIN_1; 1.

PROSITE; PS0020; WW_DOMAIN_2; 1.

PROSITE; PS50020; WW_DOMAIN_2; 1.

PROSITE; PS50020; WW_DOMAIN_2; 1.

PROSITE; PS50020; WW_DOMAIN_2; 1.
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                                                                                                                                                                                                                                                                                                                       sequences.";
d. Sci. U.S.A. 99:16899-16903(2002)
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Last sequence update)
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Pred. No. 1.4e-54;
7; Mismatches 13
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01-MAR-2004 (TrEMBLrel. 26, Last sequence upol-MAR-2004 (TrEMBLrel. 26, Last annotation a AgCP13948 (Fragment).
Name=agCG50456; ORFNames=ENSANGG0000011536;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17;
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illarity 79.0%;
Conservative 17
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PF00397; WW; 1.
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                                                                                                                                                                                                                                                                                                                                         Proc. Natl. Acad.
                                                                                                                                                                                                                                                                                                                     and mouse cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             128;
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[1] SRQUENCE

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EMBL;
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60 LLVKHSOSRRPSSWRQEKITRTKBEALELINGYIQKIKSGEEDFESLASOFSDCSSAKAR
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MRDLINE=98188272; PubMed=9520435; DOI=10.1073/pnas.95.7.3731;
Maleszka R., de Couet H.G., Miklos G.L.G.;
"Data transferability from model organisms to human beings: insights from the functional genomics of the flightless region of Drosophila.' Proc. Natl. Acad. Sci. U.S.A. 95:3731-3736(1998).
                                                                                                         IEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster (Fruit fly).

Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha, Ephydroidea, Drosophilidae, Drosophila.

NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=Oregon-R; TISSUB=Larva, and Pupae;
MEDLINE=96133954; PubMed=8552658; DOI=10.1073/pnas.93.1.447;
Maleszka R., Hanes S.D., Hackett R.L., de Couet H.G., Miklos
"The Drosophila melanogaster dodo (dod) gene, conserved in hi
functionally interchangeable with the ESS1 cell division gene
Saccharomyces cerevisiae.";
Proc. Natl. Acad. Sci. U.S.A. 93:447-451(1996).
         Anopheles Genome Sequencing Consortium;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.

-!- SIMILARITY: Belongs to the ppiC/parvulin rotamase family

-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which
preliminary data.

EMBL; AAAB01008898; EAA09299:1; -.
                                                                                                       activi
                                                                                                                                                                                                                                                 191;
                                                                                                                                                                                                                                                                                                       31 MSDGQETVPEGWEKRTSRSTGMTYYLNVYTKESQWDPPTAPAEPANTN--
                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                   189
                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                           7BD43BA02B0AD4B8 CRC64;
                                                                                HSSP; Q13526; 1F8A.
GO; GO:0016853; F:isomerase activity; IEA.
GO; GO:0003755; F:peptidyl-prolyl cis-trans isomerase
GO; GO:0006457; P:protein folding; IEA.
InterPro; IPR000297; Rotamase.
InterPro; IPR001202; WW_Rsp5_WWP.
Pfam; PF00639; Rotamase; 1.
Pfam; PF00639; WW; 1.
                                                                                                                                                                                                                                                                                                                                                                                GDIGAFSRGQMQKPFEDASFALRTGEMSGPVFTDSGIHIILR
                                                                                                                                                                                                                                                                                                                                                                                        39;
                                                                                                                                                                                                                                                 Score 491; DB 2
Pred. No. 5e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P54353; O61344; Q9VRH1;
01-OCT-1996 (Rel. 34, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
25-JAN-2005 (Rel. 46, Last annotation update)
                                                                                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                     PROSITE, PS50198; PPIC PPIASE 2; PROSITE; PS01159; WW DOMAIN 1; 1 PROSITE; PS50020; WW DOMAIN 2; 1
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                                                                                                                                                                                                                           21872 MW;
                                                                                                                                                                                                                                                 57.6%;
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                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                       Isomerase; Rotamase
                                                                                                                                                                                                                            191 AA;
                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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Name=dod; ORF
STRAIN-PEST;
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Best Local S
Matches 94
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92;
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                                                                                                                                                                                                                                                                                           MADEEKL PPGWEKRMSRSSGRVYY FNHI TNASOWERPS - - GNSSSGGKNGOGE - PARVRC
                                                                                                                                                                                                                                                                                                                            MPDARQLPDGWEKRTSRSTGMSYYLNMYTKESQWDQPTEPAKKAGGGSAGGGDAPDEVHC
                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium. Science 282:2012-2018 (1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                      161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       164
                                                                                                                                                                                                                           Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            elegans cosmid Y110A2AL.";
to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein Y110A2AL.13.
Name=Y110A2AL.13; ORFNames=Y110A2AL.13;
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      -> T (in Ref. 2).
3B4306FA930E7259 CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                    ARGULGAFSRGOMOKPFEDASFALRTGEMSGPVFTDSGIHI
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H
                                                                                                                                                                                                                        Score 456.5; DB 1;
Pred. No. 6.2e-34;
5; Mismatches 52;
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                                                                                                                                                       Ppic.
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STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
WormBase Consortium;
                           SMART; SM00456; WW; 1.
PROSITE; PS01096; PPIC_PPIASE_1;
PROSITE; PS50198; PPIC_PPIASE_2;
PROSITE; PS01159; WW_DOMAIN_1; 1
PROSITE; PS50020; WW_DOMAIN_2; 1
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                                                                                                                                                                                                                                                          16;
                                                                                                                                                                                      MW;
                                                                                                                                                                                                                       53.6%;
llarity 56.7%;
Conservative
Н
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18376
PF00639; Rotamase; PF00397; WW; 1.
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166
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Submitted (MAR-2000)
                                                                                                                     Isomerase; Rotamase.
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Submitted (MAR-2000)
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93; Conserv
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Submitted (SEF
[6]
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Q9N492;
01-OCT-2000
01-OCT-2000
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                                                                                                                                                                                     SEQUENCE
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Best Local
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4 BEKLPPGWEKRMSRSSGRVYYFNHITNASQWERPSGNSSSGGKNGQGEPARVRCSHLLVK
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SEQUENCE FROM N.A.
STRAIN=Bristol N2;
Waterston R.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
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Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases
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STRAIN=Bristol N2;
Wilson R.;
Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
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PROSITE; PS50198; PPIC PPIASE 2; 1.
PROSITE; PS50159; WW DOMAIN 1; 1.
PROSITE; PS50020; WW DOMAIN 2; 1.
Hypothetical protein; Isomerase; Rotamase.
SEQUENCE 168 AA; 19176 MW; 0FC837780579C070 CRC64;
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4.8e-32;
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STRAIN=Bristol N2;
Wilson R.;
Submitted (AUG-2004) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=Bristol N2;
WormBase Consortium;
Submitted (SEP-2004) to the EMBL/GenBank/DDBJ
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17; Mismatches
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                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=Bristol N2;
Waterston R.;
Submitted (OCT-2002) t
                                                                                                 SEQUENCE FROM N.A.
STRAIN=Bristol N2;
Waterston R.;
Submitted (JUN-2002)
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Submitted (FEB-2003)
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Submitted (NOV-2002)
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Submitted (MAY-2003)
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SEQUENCE FROM N.A.
STRAIN=Bristol N2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaffe D., Fitzhugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B., Jaffen T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M., Bikins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M., Cui D., Ianakiev P., Kinsey J.A., Braun B.L., Zelter A., Schulte U., Selitrennikoff C.P., Kinsey J.A., Braun B.L., Zelter A., Schulte U., Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D., Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D., Kamal M., Kamvysselis M., Mauceli E., Bielke C., Rudd S., Frishman D., Krystofova S., Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S., Cogoni C., Macino G., Catcheside D., Li W., Pratt R.J., Osmani S.A., DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R., Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R., Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Frettag M., Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B., Matvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Frettag M., Nature O:O-O(2003).

I. The Genome Sequence of the Filamentous Fungus Neurospora crassa.";

Nature O:O-O(2003).

I. Sachs M.S., Lander E.S., Nusbaum C., Birren B.;

REBL, Genbank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.

EMBL, AABX01000166; EAA33800.1; --

EMBL; AABX01000166; EAA33800.1; --

EMBL; AABX01000166; EAA33800.1; --

EMBL; ABXX01000166; EAA33800.1; --

EMBL; EMBL; ABXX01000166; EAA33800.1; --

EMBL; EMBL; EAUX E.S., EAUX E.S., EAUX E.S., EAUX E.S., EAUX E.S.
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 -YIOKIKSG---EEDFESLASOFSDC
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                                                                                                                                119 SSAKRGGDLGPPERRÓMÓKPPEDASPALBIGEMSDIVDTSSGVHLÍYR 166
                                                                                                                                                                                                                                                                                                                                                                                                     Neurospora crassa.
Bukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycete:
Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
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                                                                                                                                                                                                                                                                                               01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
Hypothetical protein ((AJ006023) peptidylprolyl isomerase)
                                                                                        SSAKARGDIGAFSRGOMOKPFEDASFALRTGEMSGPVFTDSGIHIILR
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PROSITE; PS01159; WW DOMAIN 1; 1.
PROSITE; PS50020; WW DOMAIN 2; 1.
Hypothetical protein; Isomerase; Rotamase.
SEQUENCE 186 AA; 21175 MW; B8E214B1E01AEA36
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ed. No. 9.2e-32;
Mismatches 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO; GO: 0016853; F: isomerase activity; IRA. GO; GO: 0003755; F: peptidyl-prolyl cis-tran GO; GO: 0006457; P: protein folding; IRA. InterPro; IPR000297; Rotamase. InterPro; IPR001202; WW_RSP5_WWP.
  HSOSRRPSSWROEKITRTKEEALELING-
                                                                                                                                                                                                                                                                                           Created)
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Pred.
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ilarity 51.1%;
Conservative 2
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(TrEMBLrel. 26, 1
(TrEMBLrel. 26, 1
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PF00397; WW; 1.
                                                                                                                                                                                                                                           PRELIMINARY;
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Best Local Similarity
Watches 91; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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01-MAR-2004
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01-MAR-2004
  64
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Pfam;
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161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biol. Chem. 273:31971-31976(1998).

1- FUNCTION: Site-specific PPIase with respect to the amino acid N-terminal to the proline residue. Peptides with glutamate, phosphoserine, or phosphothreonine in the -1 position are the best substrates. It is not only able to isomerize small peptides but is also active in protein folding.

1- CATALYTIC ACTIVITY: Peptidylproline (omega=180) = peptidylproline
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 104 BSLASQFSDCSSAKARGDLGAFSRGOMOKPFEDASFALRTGEMSGPVFTDSGIHIILR
                                 GELALTESDCSSARKRGDLGYPGRGDMQKEFEDAAFALKPGEISGIVDTASGLHLIER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            active in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND CHARACTERIZATION.
MEDLINE=99041963; PubMed=9822668; DOI=10.1074/jbc.273.48.31971;
Kops O., Eckerskorn C., Hottenrott S., Fischer G., Mi H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sordariomycetes;
Neurospora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (omega=0).
SIMILARITY: Belongs to the ppiC/parvulin rotamase family
SIMILARITY: Contains 1 WW domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tropschug M.; "Sepl, a site specific parvulin homolog from N.crassa protein folding.";
J. Biol. Chem "772.1."
                                                                                                                                                                                                                                                                                                                                                           5.2.1.8)
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Pred. No. 2.6e-31;
0; Mismatches 50;
                                                                                                                                                                                                                                                                                                                                                                                                                        Neurospora crassa.
Eukaryota; Fungi; Ascomycota; Pezizomycotina;
Sordariomycetidae; Sordariales; Sordariaceae;
NCBI_TaxID=5141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 EEKLPPGWEKRMSRSSGRVYYFNHITNASQWERPSG
                                                                                                                                                                                                      SSP1 NEUCR STANDARD; PRT; 182 AA. 060045; 10-0CT-2003 (Rel. 42, Created) 10-0CT-2003 (Rel. 42, Last sequence update) 25-0CT-2004 (Rel. 45, Last annotation update) Peptidyl-prolyl cis-trans isomerase sspl (EC Name=ssp-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gln-rich.
PpiC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00456; WW; 1.
PROSITE; PS50198; PPIC_PPIASE_2; 1
PROSITE; PS01159; WW_DOMAIN_1; 1.
PROSITE; PS50020; WW_DOMAIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000297; Rotamase.
InterPro; IPR001202; WW Rsp5 WWP
Pfam; PF00639; Rotamase; 1.
Pfam; PF00397; WW; 1.
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Similarity 50.8%;
90; Conservative 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AJ006023; CAA06818.1;
HSSP; Q13526; 1P8A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41
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182
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SEQUENCE
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Best Local
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RESULT QEUAY2

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MEDLINE=21848401; PubMed=11859360; DOI=10.1038/nature724;

MEDLINE=21848401; PubMed=11859360; DOI=10.1038/nature724;

Mood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Squaros J., Peat N., Hayles J., Baker S., Basham D., Bowman S., Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M., A Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., Holroyd S., Hornsby T., Howarth S., McDonald S., McLean J., Annes K., Jones L., Jones M., Leather S., McDonald S., McLean J., Mooney P., Moule S., Murphy L., Niblett D., Odell C., A Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E., Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S., Skelton J., Simmonds M., Squares R., Squares S., Stevens K., Tivey A., Walsh S.V., Warren T., Whitehead S., Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B., Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mulbert H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66 GKIRCSHLLVKHRDSRRPSSWREAEITRTKEBAREILRGHQERIMRGEIRLGDLAMSBSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -RVRCSHLLVKHSQSRRPSSWRQEKITRTKBEALELINGYIQKIKSGBEDFBSLASQFSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 LPAGWEVRHSNSKNLPYYPNPATRESRWEPPADTDMETLKMYMATYHSGAATYHEAPSQE
                                                                                                                                    EMBO J, 17:1315-1327(1998).

-I- SIMILARITY: Belongs to the ppiC/parvulin rotamase family.

-I- SIMILARITY: Belongs to the ppiC/parvulin rotamase family.

EMBL; AF035768; AAC49984.1; -.

HSSP; Q13526; 1P8A.

GO; GO:0016853; F:isomerase activity; IEA.

GO; GO:0006457; F:peptidyl-prolyl cis-trans isomerase activity; IEA.

GO; GO:0006457; P:protein folding; IEA.

InterPro; IPR001202; WW_Rsp5_WWP.

InterPro; IPR001202; WW_Rsp5_WWP.

Pfam; PF00639; Rotamase; I.

Pfam; PF006397; WW; 1.
                                                                                       interacts with Cdc25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CSSAKARGDLGAFSRGOMOKPFEDASFALRTGEMSGPVFTDSGIHIILRTE 163
                                   MEDLINE=98151356; PubMed=9482729; DOI=10.1093/emboj/17.5.1315; Crenshaw D.G., Yang J., Means A.R., Kornbluth S.; "The mitotic peptidyl-prolyl isomerase, Pinl, interacts with G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1D1E8376239E1309 CRC64;
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28-FEB-2003 (Rel. 41, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Peptidyl-prolyl cis-trans isomerase pin1 (BC 5.2.1.8)
Name=pin1; ORFNames=SPCC16C4.03;
Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomyces.
Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46.6%; Score 397; DB 2; I larity 48.0%; Pred. No. 1.9e-28; Conservative 24; Mismatches 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 LPPGWEKRMSRSSGRVYYFNHITNASQWERPSGNS-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS50198; PPIC PPIASE 2; PROSITE; PS01159; WW DOMAIN 1; 1. PROSITE; PS50020; WW DOMAIN 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20038 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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SEQUENCE
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EMBO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --SSGGKNGQGEPARVRCSHLLVKHSQSRRPSSWRQEKITRTKEEALELINGYIQKIKS
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RRHEESIRS
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ALTESDCSSARKRGDLGYFGRGDMQKBFBDAAFALKPGBISDIVDTASGLHLIBRLB
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
Domingos P.C., Pereira M., Castro N.S., Felipe M.S.S., Soares C.
Jesuino R.S.A.;
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
-1- SIMILARITY: Belongs to the ppiC/parvulin rotamase family.
EMBL; AY374446; AAQ83700.1; -.
GO; GO:0016853; F:isomerase activity; IEA.
GO; GO:0006457; P:protein folding; IEA.
InterPro; IPR000297; Rotamase.
InterPro; IPR001202; WW_Rsp5_WWR.
                                                                                                                                                                                                                                      05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
Peptidyl-prolyl cis/trans isomerase.
Paracoccidioides brasiliensis.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Onygenales; mitosporic Onygenales; Paracoccidioides.
NCBI_TaxID=121759;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 190
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Bukaryota, Fungi, Ascomycota, Pezizomycotina, Eurotiomycetes
Burotiales, Trichocomaceae, Emericella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N
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(Trembirel. 06, Last sequence update)
(Trembirel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 408.5; DB 2;
Pred. No. 1.9e-29;
4; Mismatches 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          710DCBEFAA9238AE
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                                                                                                                                                                     190 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00456; WW; 1.
PROSITE; PS50198; PPIC PPIASE 2;
PROSITE; PS01159; WW DOMAIN 1; 1
PROSITE; PS50020; WW DOMAIN 2; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A 47.9%;
Similarity 44.9%;
33; Conservative 2
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Pfam; PP00397; WW; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptidyl-prolyl cis/trans
Name=pinA;
                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                          (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rotamase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Burotiales; Tricho
NCBL_TaxID=162425;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ILRTE 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [1] SEQUENCE FROM N.A.
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042735;
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Query Match Best Local

Matches

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53 ARVRCSHLLVKHSQSRRPSSWRQEKITRTKEBALELINGYIQKIKSGBEDFBSLASQFSD 112
                                                                                                                                                                                                                              FUNCTION, AND SUBCRLLULAR LOCATION.
MEDLINE=21564328; PubMed=11707530;
Huang H.-K., Forsburg S.L., John U.P., O'Connell M.J., Hunter T.;
Huang H.-K., Forsburg S.L., John U.P., O'Connell M.J., Hunter T.;
"Isolation and characterization of the Pinl/Essip homologue in
Schizosaccharomyces pombe.";
J. Cell Sci. 114:3779-3788(2001).
-!- FUNCTION: Has a role in the G1/S stage transition of mitosis where it is involved in the dephosphorylation of cdc25 and weel.
-!- CATALYTIC ACTIVITY: Peptidylproline (omega=180) = peptidylproline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -XIRASHLLVKHRESRRPSSWKEEHITRSKEEARKLAEHYBOLLKSGSVSMHDLAMKESD
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         T.E
Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M. Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B., Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S. Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J., Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.; "The genome sequence of Schizosaccharomyces pombe."; [2]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: Nuclear.
SIMILARITY: Belongs to the ppiC/parvulin rotamase family SIMILARITY: Contains 1 WW domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restricuse by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-silor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CSSAKARGDLGAFSRGOMOKPFEDASFALRTGEMSGPVFTDSGIHIILR
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Pred. No. 1.1e-27;
1; Mismatches 51;
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PROSITE; PS01096; PPIC PPIASE 1; FALSE NEG.
PROSITE; PS50198; PPIC PPIASE 2; 1.
PROSITE; PS01159; WW DOMAIN 1; FALSE NEG.
PROSITE; PS50020; WW DOMAIN 2; 1.
ISOMERASE; Mitosis; Nuclear protein; Rotamase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AL031535; CAA20742.1; -.
PIR; T41093; T41093.
HSSP; Q13526; 1PIN.
GeneDB_SPombe; SPCC16C4.03; -.
InterPro; IPR000297; Rotamase.
InterPro; IPR001202; WW_RSP5_WWP.
Pfam; PF00639; Rotamase; 1.
Pfam; PF006397; WW; 1.
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19773 MW;
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Similarity 48.5%;
82; Conservative 23
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175 AA;
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